



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 09/667237

TO: Mark Shibuya
Location: REM-2A10&2C18
Art Unit: 1639
Monday, August 01, 2005

Case Serial Number: 09/667237

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Shibuya,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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160722

From: Shibuya, Mark
Sent: Wednesday, July 27, 2005 2:30 PM
To: STIC-Biotech/ChemLib
Subject: Search req. for SEQ NO:12 of 09/667,237.

Please search SEQ NO:12 of 09/667,237.

This case is before the first action on the merits.

Mark Shibuya
Art Unit 1639, Remsen 2a10, ext: 2-0806

CRPE

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: *27/05*
Date Completed: *27/05*
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *CDI*
WWW/Internet: _____
Other(Specify): _____

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STIC SEARCH RESULTS

FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

- I am an examiner in Workgroup: Example: 1610
- Relevant prior art found, search results used as follows:
- 102 rejection
 - 103 rejection
 - Cited as being of interest.
 - Helped examiner better understand the invention.
 - Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art not found:

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.

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RESULT 6
 BX470087/c
LOCUS BX470087 218404 bp DNA linear CH211-202A10 in linkage group 3,
DEFINITION complete sequence.

ACCESSION BX470087
VERSION HTG
KEYWORDS Danio rerio (zebrafish)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 218404)
AUTHORS Pelan S
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk
COMMENT Contact: zfish-help@sanger.ac.uk
 On Feb 26, 2004 this sequence version replaced gi:42820884.

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL; SWISSLINK; TREMBL; WORMPPB; Information on the WORMPPB database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormppb. Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhiqiong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-202A10 is from a CHORI-211 BAC library

VECTOR: PTARBA2C2.1.
FEATURES
source 1
 Query Match 79-5%: Score 31; DB 5; Length 218404;
 Best Local Similarity 87.2%; Pred. No. 2;
 Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
ORIGIN

Qy 1 ACTACTGCTACTGGCTGCTACTGCTACTGCTGCTGCTACT 39
 Db 28923 ACTACTGCTACTGGCTGCTACTGCTACTGCTGCTACT 28885

RESULT 7
 AC126150/c
LOCUS AC126150 241173 bp DNA linear CH230-69110, *** SEQUENCING IN PROGRESS
DEFINITION Rattus norvegicus clone CH230-69110, ** unsorted pieces.

ACCESSION AC126150
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus
ORGANISM Mammalia; Eutheria; Rodentia; Rattus; Muridae; Murinae; Rattus
 Rattus 1 (bases 1 to 241173)

REFERENCES

AUTHORS Muzy, D. Marie.; Metzger, M. Lee.; Abramzon, S.; Adams, C.; Alder, J.; Allen, C.; Allen, H.; Alsbrooks, S.; Amati, A.; Anguiano, D.; Anyalebechi, V.; Aoyagi, A.; Ayodeji, M.; Baca, E.; Baden, H.; Benahmed, F.; Baldwin, D.; Bandaranaike, D.; Barber, M.; Barnstall, M.; Barlow, M.; Biswalo, K.; Blair, J.; Blankenburg, K.; Blivch, P.; Brown, M.; Bryant, N.; Buhay, C.; Burch, P.; Burrell, K.; Calderon, E.; Cardenas, V.; Carter, K.; Cavarozzi, I.; Cesari, H.; Center, A.; Chacko, J.; Chavez, D.; Chen, G.; Chen, R.; Chen, Z.; Chu, J.; Cleveland, C.; Cockrell, R.; Cox, C.; Coyle, M.; Cree, A.; D'Souza, L.; Davila, M.L.; Davis, C.; Davy-Carroll, L.; De Andra, C.; Dedeich, D.; Delgado, O.; Denson, S.; Desram, S.; Dugan-Rocha, S.; Dunn, A.; Durbin, K.; Duval, B.; Eaves, K.; Draper, H.; Dugan-Rocha, S.; Dunn, A.; Durbin, K.; Duval, B.; Eaves, K.; Egan, J.; Escott, M.; Eugen, C.A.; Evans, T.; Far, G.; Fernandez, S.; Finley, M.; Flagg, N.; Forbes, L.; Foster, M.; Foster, P.; Fraser, C.M.; Gabisi, A.; Garcia, R.; Garcia, A.; Garner, T.; Garza, M.; Gebregeorgis, E.; Geer, K.; Gill, R.; Grady, M.; Guerra, W.; Gunaratne, P.; Haaland, W.; Hamil, C.; Hamilton, C.; Hamilton, K.; Harvey, Y.; Havlak, P.; Hawes, A.; Henderson, N.; Hernandez, J.; Hernandez, R.; Hines, S.; Hladun, S.L.; Hodges, A.; Hogues, M.; Hollins, B.; Howell, S.; Hulyk, S.; Hume, J.; Idlebird, D.; Jackson, A.; Jackson, L.; Jacob, L.; Jiang, H.; Johnson, R.; Jolivet, A.; Karwitz, S.; Kelly, S.; Khan, Z.; King, L.; Kovar, C.; Kowis, C.; Kraft, C.L.; Lebow, H.; Levay, J.; Lewis, L.; Li, Z.; Liu, J.; Liu, W.; Liu, Y.; London, P.; Longacre, S.; Lopez, J.; Loreshewa, L.; Louis, H.; Lu, X.; Lu, Y.; Lv, J.; Ma, J.; Maheshvari, M.; Mahindartne, M.; Mahmoud, M.; Mailoy, K.; Mangum, A.; Mangum, B.; Mapua, P.; Martin, K.; Martin, R.; Martinez, B.; Mawhinney, S.; McLeod, M.P.; McNeill, T.Z.; Meenin, B.; Milosavljevic, A.; Miner, G.; Minja, E.; Montemayor, J.; Moore, S.; Morgan, M.; Morris, K.; Morris, S.; Munidasa, M.; Murphy, M.; Nair, L.; Nankervis, C.; Neal, D.; Newton, D.; Ngweny, N.; Norris, S.; Nwakelomeh, O.; Okwuonu, G.; Olarnpunsaeng, A.; Pal, S.; Parks, K.; Pasternak, S.; Paul, H.; Perez, A.; Perez, L.; Pfankoch, C.; Plopper, F.; Poindexter, A.; Popovic, D.; Primus, E.; Pu, L.-L.; Puazo, M.; Quiroz, J.; Rachlin, E.; Reeves, K.; Reiser, M.A.; Reigh, R.; Reilly, B.; Reilly, M.; Ren, Y.; Reuter, M.; Richards, S.; Riggs, F.; Rives, C.; Rodkey, T.; Rojas, A.; Rose, M.; Rose, R.; Ruiz, S.; Sanders, W.; Savery, G.; Scherer, S.; Scott, G.; Shatsman, S.; Shen, H.; Shetty, J.; Shvartsbeyn, A.; Sisson, I.; Sitter, C.D.; Smajs, D.; Snead, A.; Sodergren, E.; Song, X.-Z.; Sorelle, R.; Sosa, J.; Steimle, M.; Strong, R.; Sutton, A.; Svatek, A.; Tabor, P.; Taylor, C.; Taylor, T.; Thomas, N.; Thomas, S.; Tingey, A.; Trejos, Z.; Umani, K.; Valas, R.; Vera, V.; Villasana, D.; Waltron, D.; Wang, J.; Wang, Q.; Wang, S.; Warren, J.; Warren, R.; Wei, X.; White, F.; Williams, G.; Wilson, R.; Wileczky, R.; Wooden, H.; Worley, K.; Wright, D.; Wright, R.; Wu, J.; Yaku, S.; Yen, J.; Yoon, L.; Yoon, V.; Yu, F.; Zhang, J.; Zhou, J.; Zhou, X.; Zhao, S.; Dunn, D.; von Niederhausern, A.; Weiss, R.; Smith, D.R.; Holt, R.A.; Smith, H.O.; Weinstock, G.; Gibbs, R.A.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 241173)

AUTHORS Worley, K.C.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 241173)

FEATURES	*	201549	202550: contiguous of 1002 bp in length	JOURNAL	Submitted (16-NOV-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
source	*	202551	202650: gap of unknown length	REFERENCE	8 (bases 1 to 241381)
		202551	203739: contiguous of 1089 bp in length.	AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.
Location/Qualifiers	1..203739	/organism="Rattus norvegicus"	TITLE	Direct Submission	
		/mol type="genomic DNA"	JOURNAL	Submitted (18-SEP-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	
		/db_xref="taxon:10116"	COMMENT	On Nov 16, 2002 this sequence version replaced gi:21747519.	
		/clone="CH230-228G24"		Center: Genome Center	
misc_feature		109021..111630		Center: Department Of Chemistry And Biochemistry	
		/note="wgs contig"		The University Of Oklahoma	
misc_feature		171475..172939		Center code:UOKNOR	
ORIGIN		/note="wgs contig"			
Query Match	76.3%	Score 30; DB 2;	FEATURES	Location/Qualifiers	
Best Local Similarity	86.8%	Length 203739;	Source	1..241381	
Matches	33;	Pred. No. 4.3;		/organism="Mus musculus"	
Conservative	0;	Mismatches 5;		/mol_type="genomic DNA"	
		Indels 0;		/strain="C57BL/6J"	
		Gaps 0;		/db_xref="Taxon:10090"	
Qy	2	CTACGTCTACTGGTGTAGTACTACTGCTGTGCTAGT 39		/map="7"	
AC087063	146670	CTACTACTACTGCTGTAGTACTACTGCTGTGCTAGT 146633		/clone="rp23-20047"	
Db				/clone_1ib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"	
RESULT	14				
AC087063	AC087063	241381 bp	FEATURES	Location/Qualifiers	
LOCUS	Mus musculus	DNA	Source	1..241381	
DEFINITION	clone rp23-20047	linear		/organism="Mus musculus"	
ACCESSION	AC087063	map 7		/mol_type="genomic DNA"	
VERSION	AC087063.20	strain C57BL/6J,		/strain="C57BL/6J"	
KEYWORDS	HTG.	complete		/db_xref="Taxon:10090"	
SOURCE	Mus musculus (house mouse)				
ORGANISM	:				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Qy	2	CTACTGCTACTGGTGTAGTACTACTGCTGTGCTAGT 39	ORIGIN	
1 (bases 1 to 241381)	Db	144313	CTGCTGCTGTGGTGTAGTATTCCTGCTGTGCTAGT 144350		
REFERENCE	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.	RESULT	Query Match 76.9%; Score 30; DB 10; Length 241381;		
AUTHORS		Best Local Similarity 81.8%; Pred. No. 4.3;	Matched 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;		
TITLE		DEFINITION	Rattus norvegicus clone CH230-123D20, *** SEQUENCING IN PROGRESS		
JOURNAL		ACCESSION	AC117014		
REFERENCE	2 (bases 1 to 241381)	VERSION	AC117014		
AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.	KEYWORDS	GI:25013195		
TITLE	Unpublished	SOURCE	HTGS PHASED; HTGS DRAFT; HTGS ENRICHED.		
JOURNAL		ORGANISM	Rattus norvegicus (Norway rat)		
REFERENCE	2 (bases 1 to 241381)				
AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.				
TITLE	Unpublished				
JOURNAL					
REFERENCE	3 (bases 1 to 241381)				
AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.				
TITLE	Unpublished				
JOURNAL					
REFERENCE	4 (bases 1 to 241381)				
AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.				
TITLE	Unpublished				
JOURNAL					
REFERENCE	5 (bases 1 to 241381)				
AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.				
TITLE	Unpublished				
JOURNAL					
REFERENCE	6 (bases 1 to 241381)				
AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.				
TITLE	Unpublished				
JOURNAL					
REFERENCE	7 (bases 1 to 241381)				
AUTHORS	Wu, H., Hu, P., Yang, L., Prescott, A., DeLisle, B. and Roe, B.A.				
TITLE	Unpublished				
JOURNAL					

Lorenshewa L., Loulsegued, H., Lozano, R. J., Lu X., Ma, J., Maheshwari, M., Mahindararao, M., Mahmoud, P., Martin, K., Martin, R., Martinez, E., Nangum, B., Mapua, P., McNeill, T. Z., Meenen, E., Nauhinay, S., McLeod, M. P., Miner, G., Mitja, E., Montemayor, J., Moore, S., Nairn, A., Naylor, K., Morgan, M., Morris, K., Morris, S., Manidas, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Pal, S., Parks, K., Nwakalemen, O., Okwudu, A., Olarunpagonso, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smais, D., Snead, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejo, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wieczorkiewicz, R., Woodward, H., Worley, K., Wright, D., Wright, R., Wu, J., Yekub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Smith, H.O., Weinstock, G., and Gibbs, R.A.

JOURNAL
Unpublished
REFERENCE 2 (bases 1 to 255613)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (06-Apr-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 255613)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (15-Nov-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced GI:23267317. The sequence in this assembly is combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center clone name: CH30-13D20

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 21418 bases at least Q40

Consensus quality: 218498 bases at least Q30
Estimated insert size: 220593; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length.
* (see http://www.hgsc.bcm.tmc.edu/docs/Gembank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 7122: contig of 7122 bp in length
* 7123 7222: gap of unknown length
* 7223 236393: contig of 229171 bp in length
* 236394 236493: gap of unknown length
* 236494 239610: contig of 3117 bp in length
* 239611 239710: gap of unknown length
* 239711 254301: contig of 14551 bp in length
* 254302 254401: gap of unknown length
* 254402 255613: contig of 1212 bp in length.
FEATURES
source
FEATURES
Location/Qualifiers
1. 255613
/organism="Rattus norvegicus"
/mol type="Genomic DNA"
/db_xref="Taxon:10116"
/clone="CH30-13D20"
1. 1707
/note="wgs end_extension
clone_end:T7"
/note="clone_boundary
clone_end:T7"
site:
end Sequence: BH295470#
34541. 35596
/note="wgs contig"
misc_feature
/note="clone_boundary
clone_end:SP6"
site:
end Sequence: BH295472#
229888. 232421
/note="wgs end_extension
clone_end:SP6"
misc_feature
/note="clone_boundary
clone_end:SP6"
site:
end Sequence: BH295473#
226717. 227629
/note="wgs end_extension
clone_end:SP6"
misc_feature
/note="clone_boundary
clone_end:SP6"
ORIGIN
Query Match 76.9%; Score 30; DB 2; Length 255613;
Best Local Similarity 86.8%; Prd. No. 4.2;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CTCTGTACTGGTAGTACTACTGTGGCTAGT 39
Db 62002 CTACTACTGTGCTACTACTGTGCTAGT 62039

Search completed: July 30, 2005, 07:40:53
Job time : 1564 secs

ALIGNMENTS

RESULT 1									
N	Geneseqn16b004;*								
1:	geneseqn1900s;*								
2:	geneseqn1930s;*								
3:	geneseqn2000s;*								
4:	geneseqn2001as;*								
5:	geneseqn2001bs;*								
6:	geneseqn2002as;*								
7:	geneseqn2002bs;*								
8:	geneseqn2003as;*								
9:	geneseqn2003bs;*								
10:	geneseqn2003cs;*								
11:	geneseqn2003ds;*								
12:	geneseqn2004as;*								
13:	geneseqn2004bs;*								
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.								
SUMMARIES									
result	No.	Score	Query Match	Length	DB	ID	Description		
1	39	100.0	39	4	AHH20260		Ahh20260 CJ linker	XX	XX
2	39	100.0	39	4	Aa845570		Aa845570 B cell ly	XX	XX
3	39	100.0	39	4	ACD40364		ACd40364 DNA encod	XX	XX
4	39	100.0	39	9	ACD06879		Acdo6879 Immunogen	XX	XX
5	39	100.0	39	9	ACD06137		Acdo6137 Immunogen	XX	XX
6	39	100.0	39	9	ACD45089		Acda45089 DNA encod	XX	XX
7	30	76.9	10453	13	ABD32728		Abd32728 Mouse can	XX	XX
8	29	74.4	2059	12	ADG73739		Adg73739 Aspergill	XX	XX
9	29	74.4	3438	4	AAH62788		Aah62788 Shrimp wh	XX	XX
10	29	74.4	305107	4	AAH62689		Aah62689 Shrimp wh	XX	XX
11	28.6	73.3	204803	12	ADQ97348		Adq97348 Mouse can	XX	XX
12	28.4	72.8	39	4	AHH20262		Ahh20262 CJ linker	DR	DR
13	28.4	72.8	39	4	AAS45572		Aas45572 B cell ly	DR	DR
14	28.4	72.8	39	8	ACD40366		Acda40366 DNA encod	XX	XX
15	28.4	72.8	39	9	ACD06881		Acdo6881 Immunogen	PT	PT
16	28.4	72.8	39	9	ACD06139		Acdo6139 Immunogen	PT	PT
17	28.4	72.8	39	9	ACD45091		Acda45091 DNA encod	XX	XX
18	27.8	71.3	488	9	ACR32706		Ach32706 Human end	PS	PS
19	27.8	71.3	495	10	ADF85450		Adf85450 Human end	XX	XX
20	27.8	71.3	544	12	ACB0611		Acb0611 Human end	XX	XX

This invention relates to a library of dual-domain nucleic acid molecules. The two domains in the molecules are separated and linked by a linker which is a member of a randomised library of linkers. The linkers in the library vary in size and nucleotide sequence and consist of a repeated pattern of degenerate repeated triplet nucleotides. Included in the invention is a method for the production of the library. The library is useful for producing dual domain proteins of interest that have therapeutic value, e.g., idiotype-specific vaccine for treating B-cell lymphomas. The present sequence represents a linker oligonucleotide sequence generated in an example illustrating the invention. The example concerns the generation of a tumour antigen from a patient that includes the idiotype of C_J B cell lymphoma

XX Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGGCTACTACTGGCTGTGTTAGT 39
Db 1 ACTACTGCTACTGGCTACTACTGGCTGTGTTAGT 39

RESULT 2

AAS45570 standard; DNA; 39 BP.
ID . AAS45570

XX AC AAS45570;

XX DT 18-DEC-2001 (first entry)

XX DE B cell lymphoma C_J linker library, linker nucleotide sequence #1.
XX Human; B cell lymphoma; cytostatic; immunostimulator; self-antigen;
KW tumour-specific vaccine; tumour; polyclonal immune response;
KW idiotype-specific anti-lymphoma immune response; PCR primer; ss.
XX Synthetic.
OS Homo sapiens.

XX PN WO200168682-A1.

XX PD 20-SEP-2001.

XX PF 13-OCT-2000; 2000WO-US028362.

XX PR 10-MAR-2000; 2000US-00522900.

XX PA (LARG-) LARGE SCALE BIOLOGY CORP.
(MCCO-) MCCORMICK A A.
PA (TUSE-) TUSE D.
PA (REINL-) REINL S J.
PA (LIND-) LINDBO J A.
PA (TURP-) TURPEN T H.

XX PI Reini SJ, Turpen TH;

XX DR WPI; 2001-596903/57.
DR P-PSDB; AAU29012.

XX PT Novel polypeptide vaccine produced in plants, useful for inducing an immune response to a self-antigen on the surface of certain tumor cells.

XX PS Example 2; Page 59; 89pp; English.

XX The invention relates to a novel polypeptide self-antigen (I) useful as a tumour-specific vaccine in a subject with a tumour or at risk of developing a tumour. (I) includes an epitope or epitopes unique to, or over expressed by, cells of the tumour, thereby distinguishing the tumour from all other tumours of the same or different histological type, or in the subject or in another member of the subject's species. (I) is capable of inducing an immune response in a mammal, when used as an individual-specific immunogenic product comprising (I), and as a vaccine composition useful for inducing a tumour-specific immune response, idiotype-specific anti-lymphoma immune

CC response, a polyclonal immune response to at least one idiotype of a surface immunoglobulin or a polyclonal immune response to an idiotype. CC The vaccine composition is useful for inducing a tumour-specific immune antibody response in a tumour-bearing subject or a subject who had a CC tumour e.g. B-cell lymphoma, and was treated so that no tumour is CC clinically or radiographically evident. (I) is useful for inducing a protective antitumour immune response. (I) can be produced at high CC levels, is easy to purify and can be appropriately folded to mimic the CC conformation of the native epitopes displayed at the tumour cell surface. CC AAS45529-AAS45579 represent B cell lymphoma self antigen vaccine linker CC sequences and PCR primers of the invention

XX Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 39; DB 4; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGCTACTACTGGCTGTGTTAGT 39
Db 1 ACTACTGCTACTGGCTACTACTGGCTGTGTTAGT 39

RESULT 3

ACD40364

ID ACD40364 standard; DNA; 39 BP.

XX XX AC ACD40364;

XX DT 03-SEP-2003 (first entry)

XX DE DNA encoding C_J heavy chain variable region linker #1.

XX KW Gene; ds; gene therapy; vaccine; tumour; immunoglobulin V; IgV;
CJ heavy chain; variable region; linker.

XX OS Synthetic.

XX PN US2003035807-A1.

XX PD 20-FEB-2003.

XX PP 08-FEB-2002; 2002US-00067790.

XX PR 24-SEP-1999; 99US-0155979P.

XX PR 10-MAR-2000; 2000US-00522900.

XX PA (MCCO-) MCCORMICK A A.

PA (TUSE-) TUSE D.
PA (REINL-) REINL S J.
PA (LIND-) LINDBO J A.
PA (TURP-) TURPEN T H.

XX PI McCormick AA, Tuse D, Reini SJ, Lindbo JA, Turpen TH;

XX DR WPI; 2003-492106/46.

DR P-PSDB; ABO3260.

XX PT Use of a polypeptide self-antigen as a tumor-specific vaccine.

XX PS Example 2; Page 22; 47pp; English.

CC The invention relates to a polypeptide self-antigen useful as a tumour-specific vaccine in a subject with a tumour or at risk of developing a tumour and is encoded at least in part by a nucleic acid in the cells of the tumour. The polypeptide self antigen is useful for treating or preventing tumour. The present sequence represents DNA encoding a CJ heavy chain variable region linker

CC Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 39; DB 8; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;

XX XX 10-SEP-2003 (first entry)
 XX DE DNA encoding self-antigen vaccine associated linker peptide #1.
 XX KW Self-antigen; tumour-specific vaccine; tumour; immune response;
 XX anti-tumour immune response; vaccine; B-cell lymphoma;
 XX transient viral expression; transgenic plant;
 XX variable region gene fragment; linker; ds.
 XX OS Synthetic.
 XX PN US2003039659-A1.
 XX PD 27-FEB-2003.
 XX PF 08-FEB-2002; 2002US-00067892.
 XX PR 24-SEP-1999; 99US-0155979P.
 XX 10-MAR-2000; 2000US-00522900.
 XX PA (MCCO) MCCORMICK A A.
 PA (TUSE) TUSE D.
 PA (REINL) REINL S J.
 PA (LIND) LINDBO J A.
 PA (TURP) TURPEN T H.
 XX PI McCormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
 XX DR; 2003-492153/46.
 DR P-PSDB; ABO27245.
 XX Novel polypeptide antigen which includes epitope overexpressed by tumor
 PT cells e.g. B-cell lymphoma, and is capable of inducing immune response in
 PT mammal without need for adjuvant, useful as anti-tumor vaccine component.
 XX PS Example 2; Page 21; 48PP; English.
 XX The invention describes a polypeptide self-antigen (I) useful as tumour-
 CC specific vaccine in subject with a tumour, including an epitope or
 CC epitope unique to, or overexpressed by, cells of the tumour, is produced
 CC in a cell or organism that has been transformed or transfected with the
 CC nucleic acid derived from the tumour of subject, and is capable of
 CC inducing an immune response in a mammal without a need for adjuvant or
 CC other immunostimulatory materials. (I) is useful for inducing an immune
 CC response, preferably a protective anti-tumour immune response in a
 CC mammal, preferably human. A vaccine composition comprising (I) is useful
 CC for inducing a tumour-specific immune antibody response in a tumour-
 CC bearing subject (preferably human) or a subject who had a tumour and was
 CC treated so that no tumour is clinically radiographically evident. The
 CC vaccines are preferably useful for inducing immune antibody response
 CC against B-cell lymphoma. The polypeptide is produced without the need for
 CC denaturation or renaturation. (I) is rapidly produced in plants by
 CC transient viral expression. Plant samples expressing the desired protein
 CC can be positively identified by both enzyme linked immunosorbent assay
 CC (ELISA) and Western blotting 4 weeks after molecular cloning. Thus, (I)
 CC is expressed rapidly and easily in plants. This sequence encodes a self-
 CC antigen associated linker peptide
 XX Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 39; DB 9; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ACTACTGCACTGGTGCTAGTACTGTGGGCTAGT 39
 Db 1 ACTACTGCACTGGTGCTAGTACTGTGGGCTAGT 39
 RESULT 7
 ABD32728 standard; DNA; 109453 BP.
 ID ABD32728

XX AC ABD32728;
 XX DT 18-NOV-2004 (first entry)
 XX DE Mouse cancer-associated genomic DNA MD15-016.
 XX KW Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
 KW leukaemia; lymphoma; CAP.
 XX OS Mus musculus.
 XX PN WO2004074320-A2.
 XX PD 02-SEP-2004.
 XX PF 17-FEB-2004; 2004WO-US004730.
 XX PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388318.
 PR 15-APR-2003; 2003US-00417315.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663411.
 PR 15-DEC-2003; 2003US-00737318.
 XX PA (SAGR-) SAGRES DISCOVERY INC.
 XX PI Morris DW, Malandro MS;
 XX DR; 2004-652914/63.
 XX PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX PS disclosure; seqid 313; 310PP; English.
 XX CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, hybridoma that produces the above
 monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for inhibiting the expression of a polypeptide in a test cell sample,
 CC for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukemia. There may also be used in screening for agents that modulate
 CC cancer. The present sequence is a mouse CAP genomic sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published.pat_sequences
 XX SQ Sequence 109453 BP; 29132 A; 25085 C; 24613 G; 30623 T; 0 U; 0 Other;
 SQ Score 30; DB 13; Length 109453;

DT 11-SEP-2001 (first entry)
XX Shrimp white spot Bacilliform virus (WSBV) genomic sequence.
XX Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
KW antiviral agent; gene expression; antisense construct;
KW transgenic viral resistant shrimp; ds.
XX Shrimp white spot syndrome virus.
XX OS WO20013351-A2.
XX 31-MAY-2001.
PD 08-NOV-2000; 2000WO-US0288888.
XX PR 24-NOV-1999; 99CN-00124717.
PA (PENY-) PB CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOCGNOMAX CO LTD.
XX PI Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;
XX DR WPI; 2001-355877/37.
XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus
PT (WSBV), useful for producing viral polypeptides that can be used to
PT screen for agents that are useful for treating WSBV infection.
XX Disclosure: Fig 2; 626pp; English.
XX
CC The invention provides the primary nucleotide sequence of the WSBV genome
(CC (AAH62689), predicted transcript sequences (AAH62689-AAH72839) and
CC encoded proteins (AAH81910-AAH85051) and oligonucleotide sequences
(CC (AAH62841-63160) suitable for use as primers or probes. The nucleic acid
CC molecules and proteins of the invention are useful for diagnosis and
CC monitoring viral infection, in screens for antiviral agents and for
CC monitoring viral gene expression or activity during a treatment regimen.
CC The nucleic acid molecules are also useful as antisense constructs to
CC control viral gene expression in infected cells and tissues and to create
CC transgenic viral resistant shrimp. (Updated on 06-Aug-2003 to correct OS
XX field.)
XX Sequence 305107 BP; 92042 A; 62482 C; 62635 G; 87948 T; 0 U; 0 Other;
XX
Query Match Score 74.4%; DB 4; Length 305107;
Best Local Similarity 80.5%; Pred. No. 5.5;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ACTACTGACTGGTGCCTACTACTGGTGGCTCA 37
Db 44222 ACTGCTGCTACTGCTGCTACTACTGGTGGCTCA 44186
XX
RESULT 11
ID ADQ97348 C
XX ADQ97348 Standard; DNA; 204803 BP.
AC XX
AC ADQ97348;
XX DT 07-OCT-2004 (first entry)
XX DE Mouse cancer associated sequence MD08-036, SEQ ID 325.
KW Cystostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.
OS Mus musculus.
XX PN WO2004065304-A2.
XX PD 22-JUL-2004.
XX
PF PF 22-DEC-2003; 2003WO-US041389.
PR PR 27-DEC-2002; 2002US-00330773.
PA (SAGR-) SAGRES DISCOVERY INC.
XX PI Morris DW, Malandro MS;
XX DR WPI; 2004-543781/52.
XX PT New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX PS Claim 1; SEQ ID NO 325; 199pp; English.
XX
CC The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ9804). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic formate directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 204803 BP; 55167 A; 44951 C; 46757 G; 55510 T; 0 U; 2418 Other;
XX Query Match Score 73.3%; Best Local Similarity 88.6%; Prod. No. 7.2;
XX Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CTATGCTACTGTGCTAGTAGTACTACTGGTGGCT 36
Db 92554 CTACTGCTACTGTGCTAGTAGTACTGTGCTGCT 92520
XX
RESULT 12
ID AAH20262
ID AAH20262 standard; DNA; 39 BP.
XX AC AAH20262;
XX DT 27-JUL-2001 (first entry)
XX CU linker library oligonucleotide sequence SEQ ID 16.
XX
KW Polynucleotide library; dual-domain; linker; vaccine; B-cell lymphoma;
KW ds.
XX
Synthetic.
XX OS
XX PH Key
XX CDS 1..39
FT /*tag= a
FT /partial
FT /product= "Linker"
FT /note= "No stop or start codon given!"
XX
PN WO200123543-A1.
XX PD 05-APR-2001.
XX PP 22-SEP-2000; 2000WO-US025965.
XX PR 24-SEP-1999; 99US-0155978P.
XX PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX PI Reini SJ, Lindbo JA, Turpen T;
XX DR WPI; 2001-316135/33.
DR P-PSDB; AAB97231.
XX PT Novel library of dual-domain nucleic acid molecules useful for producing B-
PT dual-domain proteins, or idiotypic scfv vaccine useful for treating B-

PT cell lymphoma.

XX Example 1; Page 34; 77pp; English.

CC This invention relates to a library of dual-domain nucleic acid molecules. The two domains in the molecules are separated and linked by a linker which is a member of a randomised library of linkers. The linkers in the library vary in size and nucleotide sequence and consist of a repeated pattern of degenerate triplet nucleotides. Included in the invention is a method for the production of the library. The library is useful for producing dual-domain proteins of interest that have therapeutic value, e.g., idotypic scFv vaccine for treating B-cell lymphomas. The present sequence represents a linker oligonucleotide sequence generated in an example illustrating the invention. The example concerns the generation of a Tumour antigen from a patient that includes the idotype of CJ B cell lymphoma

XX Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;

SQ Query Match Score 28.4%; DB 4; Length 39;

Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CTACTGGCTACTGGTGTAGTACTACTGCTGTGCTGAGT 39

Db 2 CTACTGGTGTAGTACTACTGCTACTGCTGTGCTGAGT 39

CC epitopes in their native form. (I) is capable of inducing an immune response in a mammal, when used as an individual-specific immunogenic product comprising (I); and as a vaccine composition useful for inducing a tumour-specific immune response, idiotypic specific anti-lymphoma immune response, a polyclonal immune response to at least one idotype of a surface immunoglobulin or a polyclonal immune response to an idotype. The vaccine composition is useful for inducing a tumour-specific immune response in a tumour-bearing subject or a subject who had a tumour e.g. B-cell lymphoma, and was treated so that no tumour is clinically or radiologically evident. (I) is useful for inducing a protective antitumour immune response. (I) can be produced at high levels, is easy to purify and can be appropriately folded to mimic the conformation of the native epitopes displayed at the tumour cell surface. AAS4529/AAS4579 represent B cell lymphoma self antigen vaccine linker sequences and PCR primers of the invention

XX SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;

Query Match Score 28.4%; DB 4; Length 39;

Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CTACTGGCTACTGGTGTAGTACTACTGCTGTGCTGAGT 39
Db 2 CTACTGGTGTAGTACTACTGCTACTGCTGTGCTGAGT 39

RESULT 13

ID AAS45572 standard; DNA; 39 BP.

XX AC AAS45572; XX DT 18-DEC-2001 (first entry)

XX B cell lymphoma CJ linker library, linker nucleotide sequence #3.

XX Human; B cell lymphoma; cytosatic; immunostimulator; self-antigen; KW tumour-specific vaccine; tumour; polyclonal immune response; KW idiotypic specific anti-lymphoma immune response; PCR primer; 88.
XX Synthetic.
OS Homo sapiens.
XX PN WO200168662-A1.

XX PR 20-SEP-2001.

XX PF 13-OCT-2000; 2000WO-US028362.

XX PR 10-MAR-2000; 2000US-00522900.

XX PA (LARG-) LARGE SCALE BIOLOGY CORP.

PA (MCCO/) MCCORMICK A. A.

PA (TUSe/) TUSe D.

PA (REINL) REINL S. J.

PA (LINDBO) LINDBO J. A.

PA (TURPEN) TURPEN T. H.

PI McCormick AA, TUSe D, REINL SJ, LINDBO JA, Turpen TH;

XX DR WPI:2003-492106/46.

DR P-PDB; ABO23262.

XX PT Use of a polypeptide self-antigen as a tumor-specific vaccine.

PS Example 2; Page 22; 47pp; English.
XX The invention relates to a polypeptide self-antigen useful as a tumour-specific vaccine in a subject with a tumour or at risk of developing a tumour. (I) includes an epitope or epitopes unique to, or over expressed by, cells of the tumour, thereby distinguishing the tumour from all other tumours of the same or different histological type, or in the subject or in another member of the subject's species. (I) is

CC sequences and PCR primers of the invention

XX SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;

Query Match Score 28.4%; DB 4; Length 39;

Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CTACTGGCTACTGGTGTAGTACTACTGCTGTGCTGAGT 39
Db 2 CTACTGGTGTAGTACTACTGCTACTGCTGTGCTGAGT 39

XX DT 03-SEP-2003 (first entry)

XX DE DNA encoding CJ heavy chain variable region linker #3.

XX KW Gene; ds: gene therapy; vaccine; tumour; immunoglobulin V; IgV; CJ heavy chain; variable region; linker.

XX KW Synthetic.

XX OS US200305807-A1.

XX PN US200305807-A1.

XX PD 20-FEB-2003.

XX PR 08-FEB-2002; 2002US-00067790.

XX PR 24-SEP-1999; 99US-0155979P.

PR 10-MAR-2000; 2000US-00522900.

XX PA (MCCO/) MCCORMICK A. A.

PA (TUSe/) TUSe D.

PA (REINL) REINL S. J.

PA (LINDBO) LINDBO J. A.

PA (TURPEN) TURPEN T. H.

XX PI McCormick AA, TUSe D, REINL SJ, LINDBO JA, Turpen TH;

XX DR WPI:2003-492106/46.

DR P-PDB; ABO23262.

XX PT Use of a polypeptide self-antigen as a tumor-specific vaccine.

PS Example 2; Page 22; 47pp; English.

XX The invention relates to a novel polypeptide self-antigen (I) useful as a tumour-specific vaccine in a subject with a tumour or at risk of developing a tumour. (I) includes an epitope or epitopes unique to, or over expressed by, cells of the tumour, thereby distinguishing the tumour from all other tumours of the same or different histological type, or in the subject or in another member of the subject's species. (I) is

Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;
 Query Match 72.8%; Score 28.4; DB 8; Length 39;
 Best Local Similarity 84.2%; Pred. No. 4.3;
 Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 CTACTGCTACTGGCTAGTACTGCTGTGCTAGT 39
 Db 2 CTACTGGCTAGTACTGCTGTGCTAGT 39
 Search completed: July 30, 2005, 07:14:49
 Job time : 276 secs

RESULT 15
 ACD06881
 ID ACD06881 standard; DNA; 39 BP.
 AC ACD06881;
 XX DT 06-AUG-2003 (first entry)
 XX Immunogenic single chain antibody polypeptide (scfv) linker DNA #3.
 XX KW Tumour; immunoglobulin variable region; anti-tumour; cycostatic; vaccine;
 XX self-antigen; tumour-specific vaccine; B-cell lymphoma-specific vaccine;
 XX B-cell lymphoma; single chain antibody polypeptide; scfv; ds.
 XX OS Homo sapiens.
 XX PN US2003044420-A1.
 XX PD 06-MAR-2003.
 XX PF 08-FEB-2002; 2002US-00067893.
 XX PR 24-SEP-1999; 99US-0155979P.
 XX PR 10-MAR-2000; 2000US-00522900.
 XX PA (MCCORMICK A A.
 PA (TUSE D.
 PA (REINL S J.
 PA (LINDL J A.
 PA (TURPEN T H.
 XX PI McCormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
 XX WPI; 2003-456552/13.
 XX Novel polypeptide self-antigen useful as tumor-specific vaccine in mammals, is produced in plants and mimics one or more epitopes of antigen uniquely expressed by cells of tumor.
 XX Example 2; Page 21; 47pp; English.
 XX The invention describes a polypeptide self-antigen (I) useful as a tumour -specific vaccine in a subject with a tumour or at risk of developing a tumour, encoded by a nucleic acid (NA) in the cells of the tumour, including epitope to, or overexpressed by tumour cells, produced in a cell or organism that has been transfected with NA and in a correctly folded form; and capable of inducing an immune response in a mammal. (I) is useful as a tumour-specific vaccine, especially a B-cell lymphoma-specific vaccine. A vaccine is useful for inducing a tumour-specific immune antibody response in a tumour-bearing subject, preferably human or a subject who had a tumour and was treated so that no tumour is clinically or radiographically evident, where the tumour is B-cell lymphoma. This sequence encodes a linker peptide that joins a variable heavy chain region to a variable light chain region to form a single chain antibody polypeptide useful in the tumour-specific vaccine of the invention
 XX Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;
 Query Match 72.8%; Score 28.4; DB 9; Length 39;
 Best Local Similarity 84.2%; Pred. No. 4.3;
 Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Result No.	Score	Query Match Length DB ID	Description
C 1	27.8	71.3 3376 1 US-08-320-559-29	Sequence 29, APP1
C 2	27.8	71.3 3376 3 US-08-545-860D-29	Sequence 29, APP1
C 3	27.8	71.3 3376 5 PCT-US96-196-29	Sequence 2, APP1
C 4	26.8	68.7 1534 1 US-07-973-311B-2	Sequence 3, APP1
C 5	26.4	67.7 1037 4 US-09-181-585-3	Sequence 1, APP1
C 6	26.4	67.7 1159 4 US-09-181-515-1	Sequence 2, APP1
C 7	26.4	67.7 1471 4 US-09-181-585-2	Sequence 189005,
C 8	26.2	67.2 601 4 US-09-949-016-189405	Sequence 189006,
C 9	26.2	67.2 601 4 US-09-949-016-189406	Sequence 189007,
C 10	26.2	67.2 601 4 US-09-949-016-189407	Sequence 189008,
C 11	26.2	67.2 601 4 US-09-949-016-189408	Sequence 189009,
C 12	26.2	67.2 601 4 US-09-949-016-189409	Sequence 7819, AP
C 13	26.2	67.2 825 4 US-09-248-796A-7819	Sequence 17163,
C 14	26.2	67.2 92074 4 US-09-949-016-12163	Sequence 14577,
C 15	26.2	67.2 679533 4 US-09-949-016-14577	Sequence 14578,
C 16	26.2	67.2 679533 4 US-09-949-016-14578	Sequence 468, APP
C 17	25.2	66.7 1449 4 US-09-614-221A-468	Sequence 6040, AP
C 18	24.8	64.2 939 4 US-09-248-796A-6040	Sequence 409, APP
C 19	24.8	63.6 1830 4 US-09-248-796A-409	Sequence 1859, AP
C 20	24.6	63.1 420 4 US-09-248-796A-1859	Sequence 1352,
C 21	24.6	63.1 517 4 US-09-614-211A-1352	Sequence 93967,
C 22	24.6	63.1 601 4 US-09-949-016-93964	Sequence 8852, AP
C 23	24.6	63.1 648 4 US-09-248-796A-8852	Sequence 5, APP1
C 24	24.6	63.1 1188 4 US-09-162-842-5	Sequence 8235, AP
C 25	24.6	63.1 1671 4 US-09-248-796A-8235	Sequence 5548, AP
C 26	24.6	63.1 2289 4 US-09-248-796A-5548	Sequence 2, APP1
C 27	24.6	63.1 2369 3 US-08-910-925-2	Length: 3376 base pairs

```

; TYPE: nucleic acid
; STRANDBNESS: double
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-320-559-29

Query Match    71.3%; Score 27.8; DB 1; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1..6;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
; Query 1 ACTACTGCACTGGCTAGTACTACTGGCTGCTGCTGCTACT 39
Db 765 ACTACTGCACTGGCTAGTACTACTGGCTGCTGCTGCTACT 727

RESULT 2
; Sequence 29, Application US/0845860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; - ADDRESSSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
; ADDRESS: No. 6040140ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545, 860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/327, 392
; FILING DATE: 19-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/320, 559
; FILING DATE: 11-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/062, 443
; FILING DATE: 14-MAY-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/971, 094
; FILING DATE: 30-OCT-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/888, 839
; FILING DATE: 27-MAY-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/805, 093
; FILING DATE: 11-DEC-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 33, 229
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark
; REGISTRATION NUMBER: 33, 229
; REFERENCE/DOCKET NUMBER: TUU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDBNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-545-860D-29

Query Match    71.3%; Score 27.8; DB 3; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1..6;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
; Query 1 ACTACTGCACTGGCTAGTACTACTGGCTGCTGCTACT 39
Db 765 ACTACTGCACTGGCTAGTACTACTGGCTGCTGCTACT 727

RESULT 3
PCT-US94-04496-29/c
; Sequence 29, Application PC/US9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
; ADDRESS: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark
; REGISTRATION NUMBER: 33, 229
; REFERENCE/DOCKET NUMBER: TUU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDBNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
PCT-US94-04496-29

Query Match    71.3%; Score 27.8; DB 5; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1..6;

```

RESULT 4
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 TYPE: DNA ; ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: cDNA
 OTHER INFORMATION: comprising exons E, C, and A
 US-09-181-585-3

Query Match 67.7%; Score 26.4; DB 4; Length 1037;
 Best Local Similarity 83.3%; Pred. No. 4;
 Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Lu, Yinchun
 TITLE OF INVENTION: YCI Protein, Gene, And Uses Thereof
 NUMBER OF SEQUENCES: 5

RESULT 6
 US-09-181-585-1
 Sequence 1, Application US/09181585
 Patent No. 6524791
 GENERAL INFORMATION:
 APPLICANT: Ranum, Laura P.W.
 TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
 FILE REFERENCE: 11000900101
 CURRENT APPLICATION NUMBER: US/09/181-585
 CURRENT FILING DATE: 1998-10-28
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 1159
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-181-585-1

Query Match 67.7%; Score 26.4; DB 4; Length 1159;
 Best Local Similarity 83.3%; Pred. No. 4.1;
 Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Koob, Michael
 TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
 FILE REFERENCE: 11000900101
 CURRENT APPLICATION NUMBER: US/09/181-585
 CURRENT FILING DATE: 1998-10-28
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 1159
 TYPE: DNA
 ORGANISM: Artificial Sequence
 US-09-181-585-2

Query Match 67.7%; Score 26.4; DB 4; Length 1159;
 Best Local Similarity 83.3%; Pred. No. 4.1;
 Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Ranum, Laura P.W.
 TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
 FILE REFERENCE: 11000900101
 CURRENT APPLICATION NUMBER: US/09/181-585
 CURRENT FILING DATE: 1998-10-28
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 1471
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: cDNA
 OTHER INFORMATION: comprising exons D, C, B, and A
 US-09-181-585-2

Query Match 67.7%; Score 26.4; DB 4; Length 1471;
 Best Local Similarity 83.3%; Pred. No. 4.2;
 Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Koob, Michael
 TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
 FILE REFERENCE: 11000900101
 CURRENT APPLICATION NUMBER: US/09/181-585
 CURRENT FILING DATE: 1998-10-28
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 3
 LENGTH: 1037
 LENGTH: 1136

RESULT 8
 US-09-949-016-189405/c
 Sequence 189405, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIORITY NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 189405
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-189405

Query Match 67.2%; Score 26.2; DB 4; Length 601;
 Best Local Similarity 79.5%; Pred. No. 4.4;
 Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTACTACTGCTACT 39
 Db 135 ACTACTACTATGCTACTACTACTACTGCTACTACT 97

RESULT 11
 US-09-949-016-189408/c
 Sequence 189408, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIORITY NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 189408
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-189408

Query Match 67.2%; Score 26.2; DB 4; Length 601;
 Best Local Similarity 79.5%; Pred. No. 4.4;
 Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTACTACTGCTACT 39
 Db 244 ACTACTACTATGCTACTACTACTGCTACTACTGCTACTACT 206

RESULT 9
 US-09-949-016-189406/c
 Sequence 189406, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: CL001307
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIORITY NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIORITY NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 189406
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-189406

Query Match 67.2%; Score 26.2; DB 4; Length 601;
 Best Local Similarity 79.5%; Pred. No. 4.4;
 Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTACTACTGCTACT 39
 Db 259 ACTACTACTATGCTACTACTACTGCTACTACTGCTACTACT 221

RESULT 12
 US-09-949-016-189409/c
 Sequence 189409, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: CL001307
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIORITY NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIORITY NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 189406
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-189406

Query Match 67.2%; Score 26.2; DB 4; Length 601;
 Best Local Similarity 79.5%; Pred. No. 4.4;
 Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTACTACTGCTACT 39
 Db 209 ACTACTACTATGCTACTACTACTGCTACTACTGCTACTACT 171

RESULT 10
 US-09-949-016-189407/c
 Sequence 189407, Application US/09949016

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FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
SEQ ID NO: 189409
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-189409

Query Match 67.2%; Score 26.2%; DB 4; Length 601;
Best Local Similarity 79.5%; Pred. No. 4.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGGCTCTAGTACTACTGGCTGTCTAGT 39
Db 397 ACTACTACTATGCTACTACTACTACTGCTACTACT 359

RESULT 13
Sequence 7919, Application US/09248796A
Patient No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107116.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
SEQ ID NO: 7819
LENGTH: 825
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-7819

Query Match 67.2%; Score 26.2%; DB 4; Length 825;
Best Local Similarity 79.5%; Pred. No. 4.6;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGGCTCTAGTACTACTGGCTGTCTAGT 39
Db 421 ACTACTACTATGCTACTACTGCTACTACTGCTACT 459

RESULT 14
US-09-949-016-17163
Sequence 17163, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

Query Match 67.2%; Score 26.2%; DB 4; Length 92074;
Best Local Similarity 79.5%; Pred. No. 9;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGGCTCTAGTACTACTGGCTGTCTAGT 39
Db 40991 ACTACTACTATGCTACTACTGCTACTACT 41029

RESULT 15
Sequence 016-14577/C
Patient No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 14577
LENGTH: 678533
TYPE: DNA
ORGANISM: Human
FEATURE: misc_feature
LOCATION: (1)...(678533)
NAME KEY: misc_feature
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14577

Query Match 67.2%; Score 26.2%; DB 4; Length 678533;
Best Local Similarity 79.5%; Pred. No. 12;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGGCTCTAGTACTACTGGCTGTCTAGT 39
Db 216377 ACTACTACTATGCTACTACTGCTACT 216339

Search completed: July 30, 2005, 08:17:06
Job time : 101 secs

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Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0; US-10-067-892-45

Qy 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39
Db 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39

RESULT 2
US-10-067-790-45
Sequence 45, Application US/10067790
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Alison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CANCERS
FILE REFERENCE: 18636-169194
CURRENT APPLICATION NUMBER: US/10/067,790
PRIORITY FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 60/155,579
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 45
LENGTH: 39
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (.)
OTHER INFORMATION: linker

US-10-067-790-45

Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39
Db 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39

RESULT 3
US-10-067-892-45
Sequence 45, Application US/10067892
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Alison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CANCERS
FILE REFERENCE: 18636-169194
CURRENT APPLICATION NUMBER: US/10/067,892
PRIORITY FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 45
LENGTH: 39
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (.)
OTHER INFORMATION: linker

US-10-067-892-45

Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39
Db 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39

RESULT 4
US-10-067-893-45
Sequence 45, Application US/10067893
Publication No. US200300444201
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Alison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CANCERS
FILE REFERENCE: 18636-169194
CURRENT APPLICATION NUMBER: US/10/067,893
CURRENT FILING DATE: 2002-03-08
PRIORITY APPLICATION NUMBER: US 60/155,579
PRIORITY FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 45
LENGTH: 39
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: (.)
OTHER INFORMATION: linker

US-10-067-893-45

Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39
Db 1 ACTACTGCTACTGGGCTAGTACTACTGGGTGCTAGT 39

RESULT 5
US-10-388-838-81
Sequence 81, Application US/10388818
Publication No. US20040180344A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/388,838
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastaSQ For Windows Version 4.0
SEQ ID NO 81
LENGTH: 109453
TYPE: DNA
ORGANISM: Mus musculus
US-10-388-838-81

Query Match 76.9%; Score 30; DB 19; Length 109453;
Best Local Similarity 86.8%; Pred. No. 1.4%;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OTHER INFORMATION: linker

Qy 2 CTACTGCTACTGGTGTACTACTGGTGTACTGGTGTAGT 39
Db 2294B CTGCCTGCTGGTGTGTATATTCTGCTGGTGTAGT 22985

RESULT 6
Sequence 10191, Application US/10674124A
Publication No. US20040197797A1
GENERAL INFORMATION:
APPLICANT: INOKO, Hidetoshi
APPLICANT: TAMUYA, Gen
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
FILE REFERENCE: ORIN_003CIP
CURRENT APPLICATION NUMBER: US/10/674,124A
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/257,511
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: PCT/JP00/07621
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: JP2000-112699
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: JP2002-327516
PRIOR FILING DATE: 2002-09-28
PRIOR APPLICATION NUMBER: JP2002-3883869
PRIOR FILING DATE: 2002-12-09
SEQ ID NO: 10191
LENGTH: 192
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: DIS07_10002156
FEATURE:
OTHER INFORMATION: Located on chromosome 6
OTHER INFORMATION: Distance between a terminus base of telomere on
- OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
FEATURE: sequence : 51933016
OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
OTHER INFORMATION: 5'-terminus of this base sequence : 140055
US-10-674-124A-10191

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGGTGTACTGGTGTACTACTGGTGTAGT 39
Db 122 ACTACTGGTGTACTGGTGTACTGTGTGTAGT 84

RESULT 8
US-10-719-993-1903/C
Sequence 1093, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 5542
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1903
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-1903

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGGTGTACTGGTGTACTACTGGTGTAGT 39
Db 122 ACTACTGGTGTACTGGTGTACTGTGTGTAGT 84

RESULT 9
US-10-719-993-1907/C
Sequence 1097, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1907
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-1907

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGGTGTACTGGTGTACTACTGGTGTAGT 39
Db 122 ACTACTGGTGTACTGGTGTACTGTGTGTAGT 84

RESULT 10
US-10-719-993-10972/C
Sequence 10972, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1896
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-10972

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10972
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-719-993-10972

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.6;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGGTGTAGT 39
Db 122 ACTACTGCTGCTGTGCTGCTACTGTGCTGCTACT 84

RESULT 11
US-10-442-017-16/c
Sequence 16, Application US/10442017
; Publication No. US20030215950A1
; GENERAL INFORMATION:
; APPLICANT: Battelle Memorial Institute
; ATTORNEY: Lasure, Linda L.
; APPLICANT: Dai, Ziyu
; TITLE OF INVENTION: Isolated Polynucleotides and Methods of Promoting a Morphology In
; TITLE OF INVENTION: a Fungus
; FILE REFERENCE: PA4-195
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/10/442,017
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 2059
; TYPE: DNA
; ORGANISM: Aspergillus niger
; US-10-442-017-16

Query Match 74.4%; Score 29; DB 17; Length 2059;
Best Local Similarity 86.5%; Pred. No. 1.6;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TACTGCTACTGGTGTAGTACTACTGGTGTAGT 39
Db 1396 TGCCTCTGCTAGTAGCTAGTAGCTAGTAGT 1360

RESULT 12
US-10-719-993-97/c
Sequence 97, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michelle et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 3179
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-719-993-97

Query Match 74.4%; Score 29; DB 20; Length 3179;

Best Local Similarity 82.1%; Pred. No. 1.7;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
; Sequence 95, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michelle et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-719-993-95

Query Match 74.4%; Score 29; DB 20; Length 3261;
Best Local Similarity 82.1%; Pred. No. 1.7;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGGTGTAGT 39
Db 863 ACTACTGCTGCTGTGCTACTGTGCTACTGTGCTACT 825

RESULT 13
US-10-719-993-95/c
Sequence 95, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michelle et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3637
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-719-993-96

Query Match 74.4%; Score 29; DB 20; Length 3637;
Best Local Similarity 82.1%; Pred. No. 1.8;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGGTGTAGT 39
Db 863 ACTACTGCTGCTGTGCTACTGTGCTACTGTGCTACT 825

RESULT 14
US-10-719-993-96/c
Sequence 96, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michelle et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3637
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-719-993-96

Query Match 74.4%; Score 29; DB 20; Length 3637;
Best Local Similarity 82.1%; Pred. No. 1.8;

; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6780
; LENGTH: 289730
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(289730)
; OTHER INFORMATION: n = A, T, C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6780

Query Match 74.4%; Score 29; DB 20; Length 289730;
Best Local Similarity 82.1%; Pred. No. 3.6;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGGCTCTAGTACTGCTGTGCTAGT 39
Db 214259 ACTACTGCTGCTGCTGCTGCTGCTACTGCTGTGCTACT 214221

Search completed: July 30, 2005, 08:24:04
Job time : 416 secs

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Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
 Db 371 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 333

REFERENCE
 AUTHORS Elgar, G.; Clark, M.S.; Meek, S.; Smith, S.; Warner, S.; Edwards, Y.J.; Bouchired, N.; Cottinge, A.; Yeo, G.S.; Umrania, Y.; Williams, G. and Brenner, S.

TITLE Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning

JOURNAL Genome Res. 9 (10), 960-971 (1999)

MEDLINE 99455097
 PUBMED 10523524

REFERENCE 2 (bases 1 to 619)
 AUTHORS Elgar, G.; Clark, M.; Smith, S.; Meek, S.; Warner, S.; Umrania, Y.; Williams, G. and Brenner, S.

TITLE Direct Submission

JOURNAL Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk

COMMENT Vector: PBluescript II KS

V type: phagemid
 PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.

FEATURES source
 1 . 619 /organism="Takifugu rubripes"
 /mol type="Genomic DNA"
 /db_xref="taxon:31033"
 /clone="133B16C7"
 /clone_id="cosmid 133B16"

ORIGIN

Query Match 79.5%; Score 31; DB 9; Length 619;
 Best Local Similarity 87.2%; Pred. No. 0.81;
 Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGCTAGT 39
 Db 297 ACTACTGCTACTGGTGTAGTACTACTGCTGGCTAGT 335

RESULT 4
 LOCUS FR0019522/c
 DEFINITION F.rubripes GSS sequence, clone 031C10af9, linear GSS 25-FEB-2004
 ACCESSION AL012412
 VERSION AL012412.1 GI:2678780
 KEYWORDS GSS; genome survey sequence.
 SOURCE Takifugu rubripes (Fugu rubripes)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorph; Tetraodontiformes; Tetradontoidea; Tetracodontidae; Takifugu.

REFERENCE
 AUTHORS Elgar, G.; Clark, M.S.; Meek, S.; Smith, S.; Warner, S.; Edwards, Y.J.; Bouchired, N.; Cottinge, A.; Yeo, G.S.; Umrania, Y.; Williams, G. and Brenner, S.

TITLE Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning

JOURNAL Genome Res. 9 (10), 960-971 (1999)

MEDLINE 99455097
 PUBMED 10523524

REFERENCE 2 (bases 1 to 280)
 AUTHORS Elgar, G.; Clark, M.; Smith, S.; Meek, S.; Warner, S.; Umrania, Y.; Williams, G. and Brenner, S.

TITLE Direct Submission

JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk

COMMENT Vector: PBluescript II KS

V type: phagemid
 PRIMER: KS

DESCR:

RESULT 3
 LOCUS FR0006944
 DEFINITION F.rubripes GSS sequence, clone 133B16aC7, linear GSS 25-FEB-2004
 ACCESSION 290754
 VERSION 290754.1 GI:1867968
 KEYWORDS GSS; genome survey sequence.
 SOURCE Takifugu rubripes (Fugu rubripes)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

One pass dye-terminator sequencing of cosmid cloned genomic sequence.

FEATURES

source

Location/Qualifiers
1. .280
/organism="Takifugu rubripes"
/mol_type="Genomic DNA"
/db_xref="taxon:1033;"
/clone_lib="Cosmid 031C10"

ORIGIN

Query Match 78.5%; Score 30 6; DB 9; Length 280;
Best Local Similarity 84.6%; Pred. No 1..1;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGCTGTACTACTGGCTGCTAGT 39
Db 226 ACTGCTGCTACTGGCTGTACTACTGGCTGCTAGT 188

RESULT 5

FR001363/c LOCUS FR0013693 152 bp DNA linear GSS 25-FEB-2004

DEFINITION F. rubripes GSS sequence, clone 133B16CD1, genomic survey sequence.

ACCESSION AL004319

VERSION AL004339.1 GI:2450509

KEYWORDS GSS; genome survey sequence.

SOURCE Takifugu rubripes (Pufferfish)

ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Actinopterygii; Neopeltida; Teleostei; Neoteleostei; Neotetraodontiformes;

REFERENCE 1 Elgar G., Clark M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J., Bouchireb, N., Cottage, A., Yeo, G.S., Umrana, Y., Williams, G., and Brenner, S.

TITLE Generation and analysis of 25 Mb of genomic DNA from the pufferfish Puffer rubripes by sequence scanning

JOURNAL Genome Res. 9 (10), 960-971 (1999)

JOURNAL MEDLINE 99455097

PUBMED 10523524

REBPERCE 2 (bases 1 to 152)

AUTHORS Elgar G., Clark M., Smith, S., Meek, S., Warner, S., Umrana, Y., Williams, G., and Brenner, S.

TITLE Direct Submission (09-STRP-1997) MRC Human Genome Mapping Project Resource

JOURNAL Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk

COMMENT Vector: pBluescript II KS
V type: phagemid

PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.

FEATURES

source

Location/Qualifiers
1. .152
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/mol_type="Genomic DNA"
/db_xref="taxon:31033;"
/clone="133B16CD1"
/clone_lib="cosmid 133B16"

ORIGIN

Query Match 76.9%; Score 30 9; DB 9; Length 152;
Best Local Similarity 84.6%; Pred. No 1..7;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGCTGTACTACTGGCTGCTAGT 39
Db 90 ACTGCTGCTACTGTGCTGTACTACTGGCTGCTGCTANT 52

RESULT 6

FEATURES	BZ643398	LOCUS	BZ643398	DEFINITION	OGA0H57TC 2M_0.7-1.5_KB Zea mays genomic clone ZMBBMA0111J17, genomic survey sequence.
source		ACCESSION	BZ643398	VERSION	BZ643398.1 GI:28104877
		KEYWORDS		SOURCE	Zea mays
		ORGANISM			Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidea; Andropogoneae; Zea.
		REFERENCE	1		(bases 1 to 480)
		AUTHORS	Whitelaw C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budinian, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.		
		TITLE			Consortium for Maize Genomics
		JOURNAL			Unpublished (2002)
		COMMENT			Other GSS: OGAW057TM Contact: Cathy Whitelaw
		TIGR			TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
			Tel: 301-838-5843		
			Fax: 301-838-0208		
			Email: whitelaw@tigr.org		
		SEQ PRIMER:	TF		
		CLASS:	sheared ends		
		LOCATION/QUALIFIERS			
			1. .480		
			/organism="Zea mays"		
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			/db_xref="TAXON:4577"		
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			/clone lib="2M_0.7-1.5_KB"		
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			Best Local Similarity 86.8%; Pred. No. 1..8 ; Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;		
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		Db	63 CTACTGCTACTGCTACTACTGGCTGCTACT 100		
		RESULT 7			
		AL931932/C LOCUS	AL931932		
		DEFINITION	AL931932 NAPI Anopheles gambiae mRNA clone NAPI-P87-E-03-5, mRNA sequence.		
		ACCESSION	AL931932		
		VERSION	AL931932.1 GI:24973912		
		KEYWORDS	EST.		
		SOURCE	Anopheles gambiae (African malaria mosquito)		
			Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.		
		REFERENCE	1 (bases 1 to 493)		
		AUTHORS	Christophides G.K., Blass, K., Zdobnov, E.M., Carmouche, R., Benes, V., Christophides, F.C.		
			Anopheles gambiae EST, European Molecular Biology Laboratory		
			Unpublished (2002)		
			Contact: Christophides GK		
			Fotis C. Kafatos Laboratory		
			European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany		
			Tel: +49 6221 387-140		
			Fax: +49 6221 387-306		
			Email: christof@embl-heidelberg.de		

FEATURES source	Plate: P87 row: E column: 03 . 1..493	Qy	2 CTAAGCTACTGGCTAGTACTGACTGCTGTGCTAGT 39
/organism="Anopheles gambiae" /mol_type="mRNA" /clone="NAPI-P87-E-03-5" /lab_host="E. coli DH10B" /clone_lib="NAPI".	Db 458 CTAAGCTACTGGCTAGTACTGACTGCTGTGCTAGT 421	Db 458	2 CTAAGCTACTGGCTAGTACTGACTGCTGTGCTAGT 421
/note="Vector: pMTD-PAC (Pharmacia): Site 1: NotI; Site 2: EcoRI; ESTs sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAPI is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-805."			
ORIGIN			
Query Match Similarity 76.9%; Score 30; DB 1; Length 493; Best Local Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
Qy 1 ACTACTGCTACTGGCTAGTACTGACTGCTGTGCTAGT 38			
Db 305 ACTACTGCTACTGGCTAGTACTGACTGCTGTGCTAGT 268			
RESULT 9 LOCUS BZ643413/c 843 bp DNA linear GSS 29-JAN-2003			
DEFINITION OGAON57TM 2M_0_71_5 KB Zea mays genomic clone ZMMBMa0111u17, genomic survey sequence.			
Qy 1 (bases 1 to 843)			
ACCESSION BZ643413			
VERSION BZ643413.1			
KEYWORDS GSS			
SOURCE Zea mays			
ORGANISM Zea mays			
Spelmatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Clade; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD			
Clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE Whitehead,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Rohlfing,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.			
AUTHORS			
COMMENT Unpublished (2000)			
JOURNAL Contact: Cathy Whitelaw			
TIGR 912 Medical Center Drive, Rockville, MD 20850, USA			
Tel: 301-838-3843			
Fax: 301-838-0208			
Email: whitelaw@tigr.org			
Seq primer: TR			
Class: sheared ends.			
Location/Qualifiers			
1..843			
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ORIGIN			
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Qy 1 ACTACTGCTACTGGCTAGTACTGACTGCTGTGCTAGT 39			
Db 102 ACTACTGCTACTGGCTAGTACTGACTGCTGTGCTAGT 64			
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DEFINITION F.rubripes GSS sequence, clone 181A15A3, genomic survey sequence.			
ACCESSION AL019712			
VERSION AL019712.1			
KEYWORDS Takifugu rubripes (Fugu rubripes)			
ORGANISM Actinopterygii; Neopterygii; Teleostei; Percomorpha; Tetraodontiformes; Acanthomorpha; Acanthopterygii; Tetraodontidae; Takifugu.			
REFERENCE Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J., Williams,G., and Bouchard,N., Cottage,A., Yeo,G.S., Umrania,Y.,			

- | | |
|--|------------------------------------|
| REFERENCE | Nat. Genet. 25 (2), 235-238 (2000) |
| AUTHORS | |
| TITLE | |
| JOURNAL | |
| COMMENT | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus. | |
| 1. (bases 1 to 472) | |
| Zhao,S., Nierman,W., Peldblyum,T., Malek,J., Shatman,S., Akinz,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M. | |
| Unpublished (1999) | |
| Contact: Shaying Zhao | |
| Department of Eukaryotic Genomics | |
| 2712 Medical Center Dr., Rockville, MD 20850, USA | |
| Te: 301 838 0200 | |
| Fax: 301 838 0208 | |
| Email: zhao@tigr.org | |
| Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pjiever@digene.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.html) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/db/bac/bac_end_intro.html | |
| Plate: 290 row: D column: 23 | |
| Seq. primer: T7 | |
| Class: BAC ends | |
| Location/Qualifiers | |
| 1. 472 | |
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| /db_xref="taxon:10090" | |
| /clone="RPCI-23-29D23" | |
| /sex="Female" | |
| /lab_host="BRL Life Technologies" | |
| /clone_id="RPCI-23" | |
| /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)." | |
| FEATURES source | |
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| DEFINITION CNS04NSM/C | |
| LOCUS CNS04NSM | |
| DEFINITION Tetraodon nigroviridis Genome survey sequence T7 end of clone 123M05 of library G from Tetraodon nigroviridis, genomic survey sequence. | |
| ACCESION AU299119 | |
| VERSION GI:8038260 | |
| KEYWORDS GSS; genome survey sequence. | |
| ORGANISM Tetraodon nigroviridis | |
| ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Noteleosteii; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon. | |
| REFERENCE 1. Roest Crollius,H., Jaijlon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Pizanes,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. | |
| TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence | |
| JOURNAL Nat. Genet. 25 (2), 235-238 (2000) | |
| PUBLMED 10835645 | |
| REFERENCE 2. Roest Crollius,H., Jaijlon,O., Dasilva,C., Ozouf-Costaz,C., Pizanes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. | |
| TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis | |
| JOURNAL Genome Res. 10 (7), 939-949 (2000) | |
| REFERENCE 1. Roest Crollius,H., Jaijlon,O., Dasilva,C., Ozouf-Costaz,C., Pizanes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W. and Weissenbach,J. | |
| AUTHORS Saurin,W. and Weissenbach,J. | |
| Saurin,W. and Weissenbach,J. | |
| TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence | |
| JOURNAL Genome Res. 10 (7), 939-949 (2000) | |

MDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 735)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (112-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91060 EVRY CEDEX - FRANCE (E-mail : segr@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.
FEATURES
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ORIGIN

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Query Match Score 29.4; Score 75.4%; Score 84.6%; Score 9; Length 735;
Best Local Similarity 84.6%; Pred. No. 3.1; Mismatches 0; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ACTACTGCACTGCTAGTACTACTGGCGGCCTAGT 39
Db 451. ACTACTAATCACTGCTACTACTGTGCGCTACT 413
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Job time : 2074 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	AY588386 Humulus 1
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Run on: July 30, 2005, 06:23:19 ; Search time 1555 Seconds	(without alignments)	AC13512 Rattus no
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Sequence: 1 actactgtactgttagtactactgtctgtgtatgt		AC141031 Rattus no
Scoring table: IDENTITY_NUC		AC148509 Macropus
Gapop 10.0 , Gapext 1.0		AC126695 Mus muscu
Searched: 4708233 seqs, 24227607955 residues		AC14695 Arbabia p
Total number of hits satisfying chosen parameters:	9416466	AC121681 Rattus no
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Maximum DB seq length: 2000000000		AC121428 Rattus no
Post-processing: Minimum Match 0%		AC103597 Mus muscu
Post-processing: Maximum Match 100%		AC094468 Rattus no
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3: gb_in:*		AC12926
4: gb_lom:*		AC107476
5: gb_ov:*		AC097807 Rattus no
6: gb_dat:*		AC095714 Rattus no
7: gb_ph:*		AC123012 Rattus no
8: gb_dl:*		AX151593 Sequence
9: gb_pr:*		AC073966 Homo sapi
10: gb_ro:*		AC092155 Homo sapi
11: gb_sts:*		AC023942 Homo sapi
12: gb_yy:*		AF366029 White spo
13: gb_un:*		AX151396 Sequence
14: gb_vl:*		AF332093 White spo
		ALIGNMENTS
		RESULT 1
		AX250377
	LOCUS	Sequence 45 from Patent WO0168882.
	DEFINITION	39 bp
	ACCESSION	DNA
	VERSION	linear
	KEYWORDS	PAT 05-OCT-2001
	SOURCE	
	ORGANISM	
	unidentified	
	unclassified	
	unclassified	
	REFERENCE	
	AUTHORS	Reinl,S.J. and Turpen,T.H.
	TITLE	Self antigen vaccines for treating b cell lymphomas and other cancers
	JOURNAL	Patent: WO 0168882-A 45 20-SEP-2001;
	FEATURES	Large Scale Biology Corporation (US)
	Source	Location/Qualifies
		1. .39
		/organism="unidentified"
		/mol_type="unassigned DNA"
		/db_xref="taxon:32644"
		/noFee="linker"
		ORIGIN
		Query Match 100.0%; Score 39; DB 6;
		Best Local Similarity 100.0%; Pred. No. 0.0068;
		Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Qy	1 ACTACTGCTACTGGTGTAGTACTACTGCTGTTGCTAGT 39
	Db	1 ACTACTGCTACTGGTGTAGTACTACTGCTGTTGCTAGT 39
		SUMMARIES
		Result No. Score Query Match Length DB ID Description
		- - - - - AX250377 Sequence
		AX108708 Sequence
		Continuation (18 of
		BX006190_7
		BX004814_5
		BX470087
		AC126150 Rattus no
		BV090840 RPAMMSBQ0
		AF329581 Plasmodiu
		AY375168 Plasmodiu
		AY04216 Mus muscu
		CQ86892 Sequence
		AC117361 Rattus no
		AC087063 Mus muscu
		AC117014 Rattus no
		AY39037 Human DNA
		AJ418697 Sparus au
		AB116615 Plasmodiu
		AF413050 Zea mays
		RESULT 2
		AX108708
	LOCUS	Sequence 12 from Patent WO0123543.
	DEFINITION	38 bp
	ACCESSION	DNA
	VERSION	linear
	KEYWORDS	PAT 30-APR-2001.
	SOURCE	
	ORGANISM	
		synthetic construct
		synthetic construct

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	39	100.0	39	6	AX250377	AX250377 Sequence
2	37	94.9	38	6	AX108708	AX108708 Sequence
c 3	31.6	81.0	40346	2	AP006190_7	Continuation (18 of
c 4	31.6	81.0	110000	2	AP006190_6	BX006190_7
c 5	31	79.5	17710	5	BX004814_5	BX004814 Zebrafish
c 6	31	79.5	218404	5	BX470087	BX470087 Zebrafish
c 7	30	79.5	241173	2	AC126150	AC126150 Rattus no
c 8	30	76.9	402	11	BV090840	BV090840 RPAMMSBQ0
c 9	30	76.9	410	3	AF329581	AF329581 Plasmodiu
c 10	30	76.9	558	3	AY375168	AY375168 Plasmodiu
c 11	30	76.9	5460	10	AY04216	AY04216 Mus muscu
c 12	30	76.9	109453	6	CQ86892	CQ86892 Sequence
c 13	30	76.9	201739	2	AC117361	AC117361 Rattus no
c 14	30	76.9	241381	10	AC087063	AC087063 Mus muscu
c 15	30	76.9	255613	2	AC117014	AC117014 Rattus no
c 16	29.6	75.9	79531	9	AY39037	AY39037 Human DNA
c 17	29.4	75.4	420	5	SAU418697	AJ418697 Sparus au
c 18	29.4	75.4	533	3	AB116615	AB116615 Plasmodiu
c 19	29.4	75.4	543	8	AF413050	AF413050 Zea mays

REFERENCE	Other sequences; artificial sequences.
AUTHORS	Reinl,S.J., Lindbo,J.A. and Turpen,T.
TITLE	Creation of variable length and sequence linker regions for dual-domain or multi-domain molecules
JOURNAL	Patent: WO 012543-A 12-05-APR-2001;
FEATURES	Large Scale Biology Corporation (US)
source	Location/Qualifiers 1. .38 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:12630" /note="Linker region nucleotide sequence"
ORIGIN	
Query Match	94.9%; Score 37; DB 6; Length 38; Best Local Similarity 100.0%; Pred. No. 0.033; 0; Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 TACTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 39
Db	2 TACTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 38
RESULT 3	
AP006490_7/c	
WPCOMMENT	
Sequence split into 8 fragments LOCUS AP006490 Accession AP006490	
Fragment Name	Begin End
AP006490_0	1 110000
AP006490_1	100001 210000
AP006490_2	200001 310000
AP006490_3	300001 410000
AP006490_4	400001 510000
AP006490_5	500001 610000
AP006490_6	600001 710000
AP006490_7	700001 740346
Continuation (8 of 8) of AP006490 from base 700001 (AP006490 Cyanidioschyzon merolae str	
Query Match	81.0%; Score 31; DB 2; Length 40346; Best Local Similarity 89.5%; Pred. No. 1.4; Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	2 CTACTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 39
Db	49322 CTACTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 4895
RESULT 4	
AP006490_6/c	
WPCOMMENT	
Sequence split into 8 fragments LOCUS AP006490 Accession AP006490	
Fragment Name	Begin End
AP006490_0	1 110000
AP006490_1	100001 210000
AP006490_2	200001 310000
AP006490_3	300001 410000
AP006490_4	400001 510000
AP006490_5	500001 610000
AP006490_6	600001 710000
AP006490_7	700001 740346
Continuation (7 of 8) of AP006490 from base 600001 (AP006490 Cyanidioschyzon merolae str	
Query Match	81.0%; Score 31; DB 2; Length 110000; Best Local Similarity 89.5%; Pred. No. 1.3; Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	2 CTACTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 39
Db	104932 CTACTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 104895
RESULT 5	

BX004814/C BX004814 LOCUS BX004814 DEFINITION Zebratfish DNA sequence from clone CH211-10316 in linkage group 1, complete sequence.
 ACCESSION BX004814
 VERSION BX004814.8 GI:39540497 HTG.
 KEYWORDS
 SOURCE Danio rerio (zebratfish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 REFERENCE 1 (bases 1 to 171710)
 AUTHORS Howden, P.
 TITLE Direct Submission
 JOURNAL Submitted (06-DBC-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk
 COMMENT On Dec 6, 2003 this sequence version replaced gi:31620701.
 CENTER Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclones; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TRIMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by the Recon repeat discovery system (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_reario/fishmask.shtml CH211-10316 is from a CHORI-211 BAC library VBCtor: pTARBAC2.1 Clone-derived Zebratfish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

FEATURES	source	Location/Qualifiers
1. .171710		/organism="Danio rerio" /mol_type="genomic DNA" /db_xref="Taxon:7955" /clone="CH211-10316" /clone_lib="CHORI-211"

Query Match 79.5%; Score 31; DB 5; Length 171710;
 Best Local Similarity 87.2%; Pred. No. 2;
 Matches 34; Conservate 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 39
 Db 58965 ACTAGTGCTACTGGCTAGTACTATGGCGTGTGCTAGT 58927